

#2

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,717

DATE: 01/15/2002

TIME: 07:48:10

Input Set : A:\Es.txt

Output Set: N:\CRF3\01152002\J032717.raw

**ENTERED**

4 <110> APPLICANT: Andre R. Abad  
 5 Nicholas B. Duck  
 6 Xiang Feng  
 7 Ronald D. Flannagan  
 8 Theodore W. Kahn  
 9 Lynn E. Sims  
 11 <120> TITLE OF INVENTION: Genes Encoding Novel Proteins With  
 12 Pesticidal Activity Against Coleopterans  
 15 <130> FILE REFERENCE: 35718/237005  
 17 <140> CURRENT APPLICATION NUMBER: US/10/032,717  
 17 <141> CURRENT FILING DATE: 2001-10-23  
 17 <150> PRIOR APPLICATION NUMBER: 60/242,838  
 18 <151> PRIOR FILING DATE: 2000-10-24  
 20 <160> NUMBER OF SEQ ID NOS: 48  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 3621  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Bacillus thuringiensis  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (1)...(3621)  
 33 <221> NAME/KEY: misc\_feature  
 34 <222> LOCATION: (0)...(0)  
 35 <223> OTHER INFORMATION: Cry1218-1  
 37 <400> SEQUENCE: 1  
 38 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
 39 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 40 1 5 10 15  
 42 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 43 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 44 20 25 30  
 46 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 47 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 48 35 40 45  
 50 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 51 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 52 50 55 60  
 54 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240  
 55 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 56 65 70 75 80  
 58 cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288  
 59 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 60 85 90 95  
 62 act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336  
 63 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 64 100 105 110

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66 gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
67 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
68      115      120      125
70 gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
71 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
72      130      135      140
74 aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480
75 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
76 145      150      155      160
78 aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
79 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
80      165      170      175
82 gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat ttt 576
83 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
84      180      185      190
86 gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat tta 624
87 Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu
88      195      200      205
90 ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg tca 672
91 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser
92      210      215      220
94 aca act act att aat aac tat tat gat cgt caa atg aaa ctt act gca 720
95 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
96 225      230      235      240
98 gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa 768
99 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
100      245      250      255
102 tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc cgt 816
103 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
104      260      265      270
106 aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca aat 864
107 Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn
108      275      280      285
110 tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg 912
111 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
112      290      295      300
114 gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt 960
115 Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
116 305      310      315      320
118 tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt 1008
119 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
120      325      330      335
122 att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat 1056
123 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
124      340      345      350
126 aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct 1104
127 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
128      355      360      365
130 ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt caa 1152

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131 Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln
132      370      375      380
134 caa atg tat gga act aat caa aat cta cac agc act agt acc ttt gat 1200
135 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
136 385      390      395      400
138 ttt acg aat tat gat att tac aag act cta tca aag gat gca gta ctc 1248
139 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
140      405      410      415
142 ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg cca 1296
143 Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
144      420      425      430
146 gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg 1344
147 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
148      435      440      445
150 tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga gat 1392
151 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp
152      450      455      460
154 tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag 1440
155 Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu
156 465      470      475      480
158 tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt 1488
159 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly
160      485      490      495
162 aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt gca 1536
163 Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala
164      500      505      510
166 gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg gcc 1584
167 Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala
168      515      520      525
170 gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga cca 1632
171 Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro
172      530      535      540
174 gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct 1680
175 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser
176 545      550      555      560
178 gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa gca 1728
179 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala
180      565      570      575
182 ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att gta 1776
183 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val
184      580      585      590
186 ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca 1824
187 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro
188      595      600      605
190 ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca 1872
191 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr
192      610      615      620
194 aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta 1920
195 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu

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196 625          630          635          640
198 ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga 1968
199 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg
200          645          650          655
202 atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa caa gat tta 2016
203 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu Gln Asp Leu
204          660          665          670
206 gaa gca gcg aag aaa gca gtg aat gcc ttg ttt acg aat aca aaa gat 2064
207 Glu Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr Asn Thr Lys Asp
208          675          680          685
210 ggc tta cga cca ggc gta acg gat tat gaa gtg aat caa gcg gca aac 2112
211 Gly Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn Gln Ala Ala Asn
212          690          695          700
214 tta gtg gaa tgc cta tcg gat gat ttg tat cca aat gaa aaa cga ttg 2160
215 Leu Val Glu Cys Leu Ser Asp Asp Leu Tyr Pro Asn Glu Lys Arg Leu
216 705          710          715          720
218 tta ttt gat gca gtg aga gag gca aaa cgc ctc agt gag gca cgt aat 2208
219 Leu Phe Asp Ala Val Arg Glu Ala Lys Arg Leu Ser Glu Ala Arg Asn
220          725          730          735
222 ttg ctt caa gat cca gat ttc caa gag ata aat gga gaa aat ggc tgg 2256
223 Leu Leu Gln Asp Pro Asp Phe Gln Glu Ile Asn Gly Glu Asn Gly Trp
224          740          745          750
226 acg gca agt acg gga att gag gtt ata gaa ggg gat gct tta ttc aaa 2304
227 Thr Ala Ser Thr Gly Ile Glu Val Ile Glu Gly Asp Ala Leu Phe Lys
228          755          760          765
230 ggg cgt tat cta cgc cta cca ggt gcg aga gaa ata gat acg gaa acg 2352
231 Gly Arg Tyr Leu Arg Leu Pro Gly Ala Arg Glu Ile Asp Thr Glu Thr
232          770          775          780
234 tat cca acg tat ctg tat caa aaa gta gag gaa ggt gta tta aaa cca 2400
235 Tyr Pro Thr Tyr Leu Tyr Gln Lys Val Glu Gly Val Leu Lys Pro
236 785          790          795          800
238 tac aca aga tat aga ttg aga ggg ttt gtc gga agc agt caa gga ttg 2448
239 Tyr Thr Arg Tyr Arg Leu Arg Gly Phe Val Gly Ser Ser Gln Gly Leu
240          805          810          815
242 gaa att ttc aca att cgt cat caa acg aac cga att gta aaa aat gta 2496
243 Glu Ile Phe Thr Ile Arg His Gln Thr Asn Arg Ile Val Lys Asn Val
244          820          825          830
246 ccg gat gat ttg ctg cca gat gta tct cct gtt aac tcg gat ggt agt 2544
247 Pro Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn Ser Asp Gly Ser
248          835          840          845
250 atc aat cga tgc agc gaa caa aag tat gtg aat agc cgt tta gaa gta 2592
251 Ile Asn Arg Cys Ser Glu Gln Lys Tyr Val Asn Ser Arg Leu Glu Val
252          850          855          860
254 gaa aac cgt tot ggt gaa gcg cat gag ttc tct att cct att gat aca 2640
255 Glu Asn Arg Ser Gly Glu Ala His Glu Phe Ser Ile Pro Ile Asp Thr
256 865          870          875          880
258 ggt gaa atc gat tac aat gaa aat gca gga ata tgg gtt gga ttt aag 2688
259 Gly Glu Ile Asp Tyr Asn Glu Asn Ala Gly Ile Trp Val Gly Phe Lys
260          885          890          895

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262 att acg gac cca gag gga tat gca aca ctc gga aac cta gaa ttg gtc 2736
263 Ile Thr Asp Pro Glu Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val
264          900          905          910
266 gaa gag gga cct tta tca gga gac gca tta gaa cgc ttg caa aga gaa 2784
267 Glu Glu Gly Pro Leu Ser Gly Asp Ala Leu Glu Arg Leu Gln Arg Glu
268          915          920          925
270 gaa caa cag tgg aag att caa atg aca aga aga cgt gaa gaa aca gat 2832
271 Glu Gln Gln Trp Lys Ile Gln Met Thr Arg Arg Arg Glu Glu Thr Asp
272          930          935          940
274 aga agg tat atg gca tcg aaa caa gcg gta gat cgt tta tat gcc gat 2880
275 Arg Arg Tyr Met Ala Ser Lys Gln Ala Val Asp Arg Leu Tyr Ala Asp
276 945          950          955          960
278 tat cag gat cag caa ctg aat cct gat gta gag att aca gat ctt act 2928
279 Tyr Gln Asp Gln Gln Leu Asn Pro Asp Val Glu Ile Thr Asp Leu Thr
280          965          970          975
282 gcg gcc caa gat ctg ata cag tcc att cct tac gta tat aac gaa atg 2976
283 Ala Ala Gln Asp Leu Ile Gln Ser Ile Pro Tyr Val Tyr Asn Glu Met
284          980          985          990
286 ttc cca gaa ata cca ggg atg aac tat acg aag ttt aca gaa tta aca 3024
287 Phe Pro Glu Ile Pro Gly Met Asn Tyr Thr Lys Phe Thr Glu Leu Thr
288          995          1000          1005
290 gat cga ctc caa caa gcg tgg agt ttg tat gat cag cga aat gcc ata 3072
291 Asp Arg Leu Gln Gln Ala Trp Ser Leu Tyr Asp Gln Arg Asn Ala Ile
292          1010          1015          1020
294 cca aat ggt gat ttt cga aat ggg tta agt aat tgg aat gca acg cct 3120
295 Pro Asn Gly Asp Phe Arg Asn Gly Leu Ser Asn Trp Asn Ala Thr Pro
296 1025          1030          1035          1040
298 ggc gta gaa gta caa caa atc aat cat aca tct gtc ctt gtg att cca 3168
299 Gly Val Glu Val Gln Gln Ile Asn His Thr Ser Val Leu Val Ile Pro
300          1045          1050          1055
302 aac tgg gat gag caa gtt tcg caa cag ttt aca gtt caa ccg aat caa 3216
303 Asn Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val Gln Pro Asn Gln
304          1060          1065          1070
306 aga tat gtg tta cga gtt act gcg aga aaa gaa ggg gta gga aat gga 3264
307 Arg Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly Val Gly Asn Gly
308          1075          1080          1085
310 tat gta agt atc cgt gat ggt gga aat caa aca gaa acg ctt act ttt 3312
311 Tyr Val Ser Ile Arg Asp Gly Gly Asn Gln Thr Glu Thr Leu Thr Phe
312          1090          1095          1100
314 agt gca agc gat tat gat aca aat gga atg tat aat acg caa gtg tcc 3360
315 Ser Ala Ser Asp Tyr Asp Thr Asn Gly Met Tyr Asn Thr Gln Val Ser
316 1105          1110          1115          1120
318 aat aca aat gga tat aac aca aat aat gcg tat aat aca caa gca tcg 3408
319 Asn Thr Asn Gly Tyr Asn Thr Asn Asn Ala Tyr Asn Thr Gln Ala Ser
320          1125          1130          1135
322 agt aca aac gga tat aac gca aat aat atg tat aat acg caa gca tcg 3456
323 Ser Thr Asn Gly Tyr Asn Ala Asn Asn Met Tyr Asn Thr Gln Ala Ser
324          1140          1145          1150
326 aat aca aac gga tat aac aca aat agt gtg tac aat gat caa acc ggc 3504

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/032,717

DATE: 01/15/2002

TIME: 07:48:11

Input Set : A:\Es.txt

Output Set: N:\CRF3\01152002\J032717.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No  
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date